

Application No.: 09/015,399

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

• For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/015,399DATE: 03/26/1999
TIME: 14:04:59

INPUT SET: S31206.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Hinkkanen, Ari

(ii) TITLE OF INVENTION: A New Fusion Protein and Its Use in an
Immunoassay for the Simultaneous Detection of
Autoantibodies Related to Insulin-Dependent Diabetes
Mellitus

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
(B) STREET: 555 Thirteenth Street N.W., Suite 701-E
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/015,399
(B) FILING DATE: 29-JAN-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ihnen, Jeffrey L.
(B) REGISTRATION NUMBER: 28,957
(C) REFERENCE/DOCKET NUMBER: 2328-111

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-783-6040
(B) TELEFAX: 202-783-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

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47 (B) TYPE: amino acid
48 (C) STRANDEDNESS:
49 (D) TOPOLOGY: linear
50
51 (ii) MOLECULE TYPE: peptide
52
53 (v) FRAGMENT TYPE: N-terminal
54
55
56
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60 Asp Tyr Lys Asp Asp Asp Lys
61 1 5
62
63 (2) INFORMATION FOR SEQ ID NO:2:
64
65 (i) SEQUENCE CHARACTERISTICS:
66 (A) LENGTH: 9 amino acids
67 (B) TYPE: amino acid
68 (C) STRANDEDNESS:
69 (D) TOPOLOGY: linear
70
71 (ii) MOLECULE TYPE: peptide
72
73 (v) FRAGMENT TYPE: internal
74
75
76
77
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
79
80 Lys Lys Lys Arg Pro Arg Lys Lys Lys
81 1 5
82
83 (2) INFORMATION FOR SEQ ID NO:3:
84
85 (i) SEQUENCE CHARACTERISTICS:
86 (A) LENGTH: 10 amino acids
87 (B) TYPE: amino acid
88 (C) STRANDEDNESS:
89 (D) TOPOLOGY: linear
90
91 (ii) MOLECULE TYPE: peptide
92
93 (v) FRAGMENT TYPE: C-terminal
94
95
96
97
98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
99

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100 Cys Asn Gly Ser His His His His His His
101 1 5 10
102

103 (2) INFORMATION FOR SEQ ID NO:4:
104

105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 9 amino acids
107 (B) TYPE: amino acid
108 (C) STRANDEDNESS:
109 (D) TOPOLOGY: linear
110

111 (ii) MOLECULE TYPE: peptide
112

113 (v) FRAGMENT TYPE: internal
114
115
116
117

118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
119

120 Lys Lys Lys Arg Ser Arg Lys Lys Lys
121 1 5
122

123 (2) INFORMATION FOR SEQ ID NO:5:
124

125 (i) SEQUENCE CHARACTERISTICS:
126 (A) LENGTH: 979 amino acids
127 (B) TYPE: amino acid
128 (C) STRANDEDNESS:
129 (D) TOPOLOGY: linear
130

131 (ii) MOLECULE TYPE: protein
132
133
134
135

136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
137

138 Met Arg Arg Pro Arg Arg Pro Gly Gly Leu Gly Gly Ser Gly Gly Leu
139 1 5 10 15
140

141 Arg Leu Leu Leu Cys Leu Leu Leu Leu Ser Ser Arg Pro Gly Gly Cys
142 20 25 30
143

144 Ser Ala Val Ser Ala His Gly Cys Leu Phe Asp Arg Arg Leu Cys Ser
145 35 40 45
146

147 His Leu Glu Val Cys Ile Gln Asp Gly Leu Phe Gly Gln Cys Gln Val
148 50 55 60
149

150 Gly Val Gly Gln Ala Arg Pro Leu Leu Gln Val Thr Ser Pro Val Leu
151 65 70 75 80
152

RAW SEQUENCE LISTING PATENT APPLICATION US/09/015,399

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153	Gln Arg Leu Gln Gly Val Leu Arg Gln Leu Met Ser Gln Gly Leu Ser	
154		85 90 95
155		
156	Trp His Asp Asp Leu Thr Gln Tyr Val Ile Ser Gln Glu Met Glu Arg	
157		100 105 110
158		
159	Ile Pro Arg Leu Arg Pro Pro Glu Pro Arg Pro Arg Asp Arg Ser Gly	
160		115 120 125
161		
162	Leu Ala Pro Lys Arg Pro Gly Pro Ala Gly Glu Leu Leu Leu Gln Asp	
163		130 135 140
164		
165	Ile Pro Thr Gly Ser Ala Pro Ala Ala Gln His Arg Leu Pro Gln Pro	
166		145 150 155 160
167		
168	Pro Val Gly Lys Gly Gly Ala Gly Ala Ser Ser Ser Leu Ser Pro Leu	
169		165 170 175
170		
171	Gln Ala Glu Leu Leu Pro Pro Leu Leu Glu His Leu Leu Leu Pro Pro	
172		180 185 190
173		
174	Gln Pro Pro His Pro Ser Leu Ser Tyr Glu Pro Ala Leu Leu Gln Pro	
175		195 200 205
176		
177	Tyr Leu Phe His Gln Phe Gly Ser Arg Asp Gly Ser Arg Val Ser Glu	
178		210 215 220
179		
180	Gly Ser Pro Gly Met Val Ser Val Gly Pro Leu Pro Lys Ala Glu Ala	
181		225 230 235 240
182		
183	Pro Ala Leu Phe Ser Arg Thr Ala Ser Lys Gly Ile Phe Gly Asp His	
184		245 250 255
185		
186	Pro Gly His Ser Tyr Gly Asp Leu Pro Gly Pro Ser Pro Ala Gln Leu	
187		260 265 270
188		
189	Phe Gln Asp Ser Gly Leu Leu Tyr Leu Ala Gln Glu Leu Pro Ala Pro	
190		275 280 285
191		
192	Ser Arg Ala Arg Val Pro Arg Leu Pro Glu Gln Gly Ser Ser Ser Arg	
193		290 295 300
194		
195	Ala Glu Asp Ser Pro Glu Gly Tyr Glu Lys Glu Gly Leu Gly Asp Arg	
196		305 310 315 320
197		
198	Gly Glu Lys Pro Ala Ser Pro Ala Val Gln Pro Asp Ala Ala Leu Gln	
199		325 330 335
200		
201	Arg Leu Ala Ala Val Leu Ala Gly Tyr Gly Val Glu Leu Arg Gln Leu	
202		340 345 350
203		
204	Thr Pro Glu Gln Leu Ser Thr Leu Leu Thr Leu Leu Gln Leu Leu Pro	
205		355 360 365

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206																	
207	Lys	Gly	Ala	Gly	Arg	Asn	Pro	Gly	Gly	Val	Val	Asn	Val	Gly	Ala	Asp	
208		370					375					380					
209																	
210	Ile	Lys	Lys	Thr	Met	Glu	Gly	Pro	Val	Glu	Gly	Arg	Asp	Thr	Ala	Glu	
211		385				390					395					400	
212																	
213	Leu	Pro	Ala	Arg	Thr	Ser	Pro	Met	Pro	Gly	His	Pro	Thr	Ala	Ser	Pro	
214					405					410					415		
215																	
216	Thr	Ser	Ser	Glu	Val	Gln	Gln	Val	Pro	Ser	Pro	Val	Ser	Ser	Glu	Pro	
217				420					425					430			
218																	
219	Pro	Lys	Ala	Ala	Arg	Pro	Pro	Val	Thr	Pro	Val	Leu	Leu	Glu	Lys	Lys	
220			435					440					445				
221																	
222	Ser	Pro	Leu	Gly	Gln	Ser	Gln	Pro	Thr	Val	Ala	Gly	Gln	Pro	Ser	Ala	
223		450					455					460					
224																	
225	Arg	Pro	Ala	Ala	Glu	Glu	Tyr	Gly	Tyr	Ile	Val	Thr	Asp	Gln	Lys	Pro	
226		465				470					475					480	
227																	
228	Leu	Ser	Leu	Ala	Ala	Gly	Val	Lys	Leu	Leu	Glu	Ile	Leu	Ala	Glu	His	
229					485					490					495		
230																	
231	Val	His	Met	Ser	Ser	Gly	Ser	Phe	Ile	Asn	Ile	Ser	Val	Val	Gly	Pro	
232				500					505					510			
233																	
234	Ala	Leu	Thr	Phe	Arg	Ile	Arg	His	Asn	Glu	Gln	Asn	Leu	Ser	Leu	Ala	
235			515					520					525				
236																	
237	Asp	Val	Thr	Gln	Gln	Ala	Gly	Leu	Val	Lys	Ser	Glu	Leu	Glu	Ala	Gln	
238		530					535					540					
239																	
240	Thr	Gly	Leu	Gln	Ile	Leu	Gln	Thr	Gly	Val	Gly	Gln	Arg	Glu	Glu	Ala	
241		545				550					555					560	
242																	
243	Ala	Ala	Val	Leu	Pro	Gln	Thr	Ala	His	Ser	Thr	Ser	Pro	Met	Arg	Ser	
244					565					570					575		
245																	
246	Val	Leu	Leu	Thr	Leu	Val	Ala	Leu	Ala	Gly	Val	Ala	Gly	Leu	Leu	Val	
247				580					585					590			
248																	
249	Ala	Leu	Ala	Val	Ala	Leu	Cys	Val	Arg	Gln	His	Ala	Arg	Gln	Gln	Asp	
250			595					600					605				
251																	
252	Lys	Glu	Arg	Leu	Ala	Ala	Leu	Gly	Pro	Glu	Gly	Ala	His	Gly	Asp	Thr	
253		610					615					620					
254																	
255	Thr	Phe	Glu	Tyr	Gln	Asp	Leu	Cys	Arg	Gln	His	Met	Ala	Thr	Lys	Ser	
256		625				630					635					640	
257																	
258	Leu	Phe	Asn	Arg	Ala	Glu	Gly	Pro	Pro	Glu	Pro	Ser	Arg	Val	Ser	Ser	

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SEQUENCE VERIFICATION REPORT
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Original Text